

47

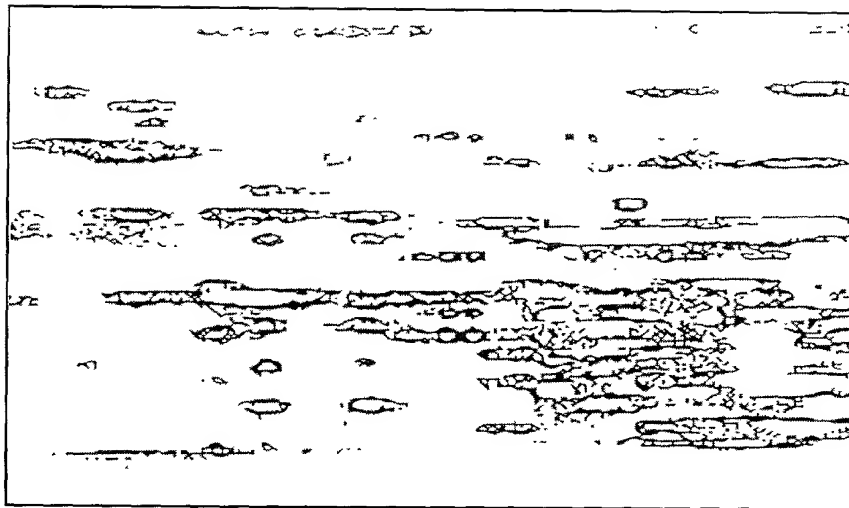


FIG. 1A

09/983,020

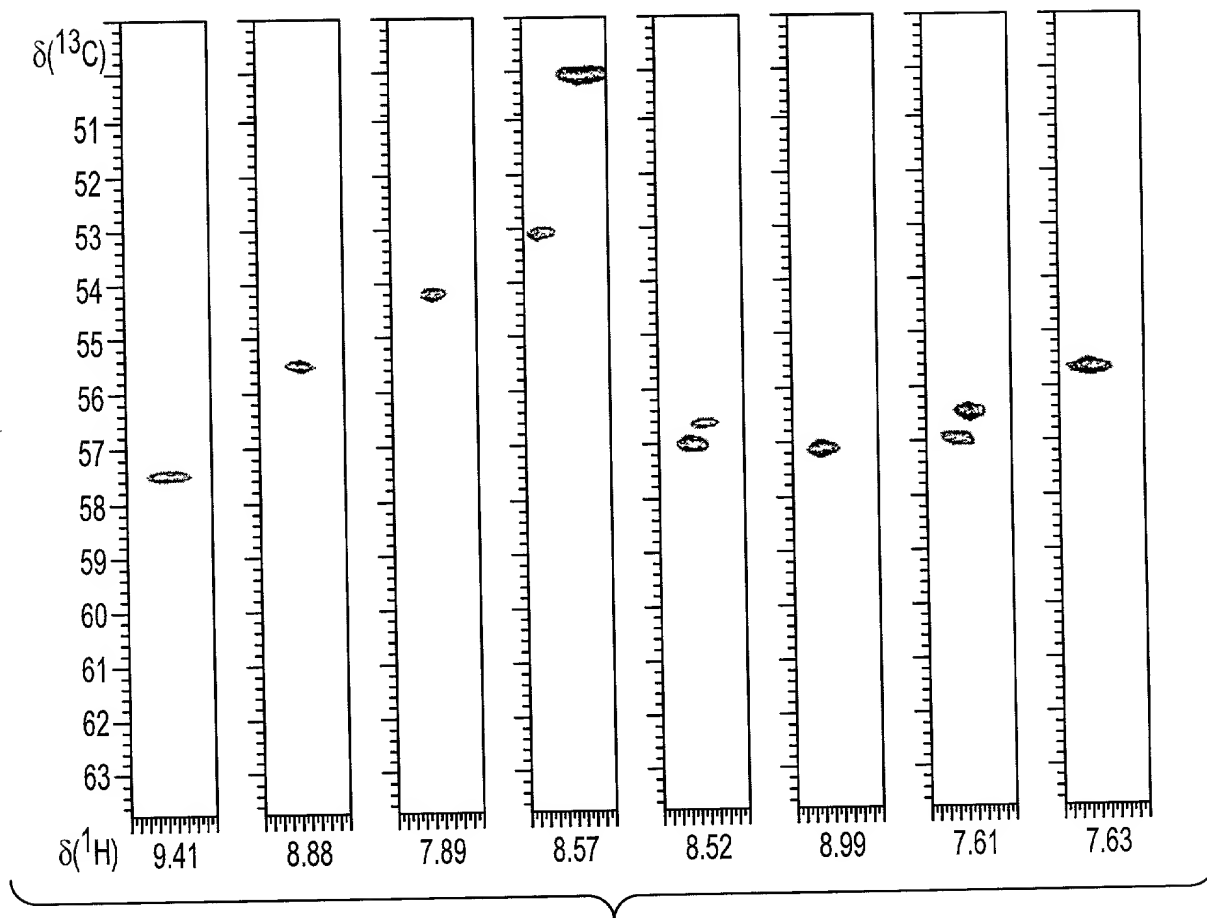


FIG. 1B

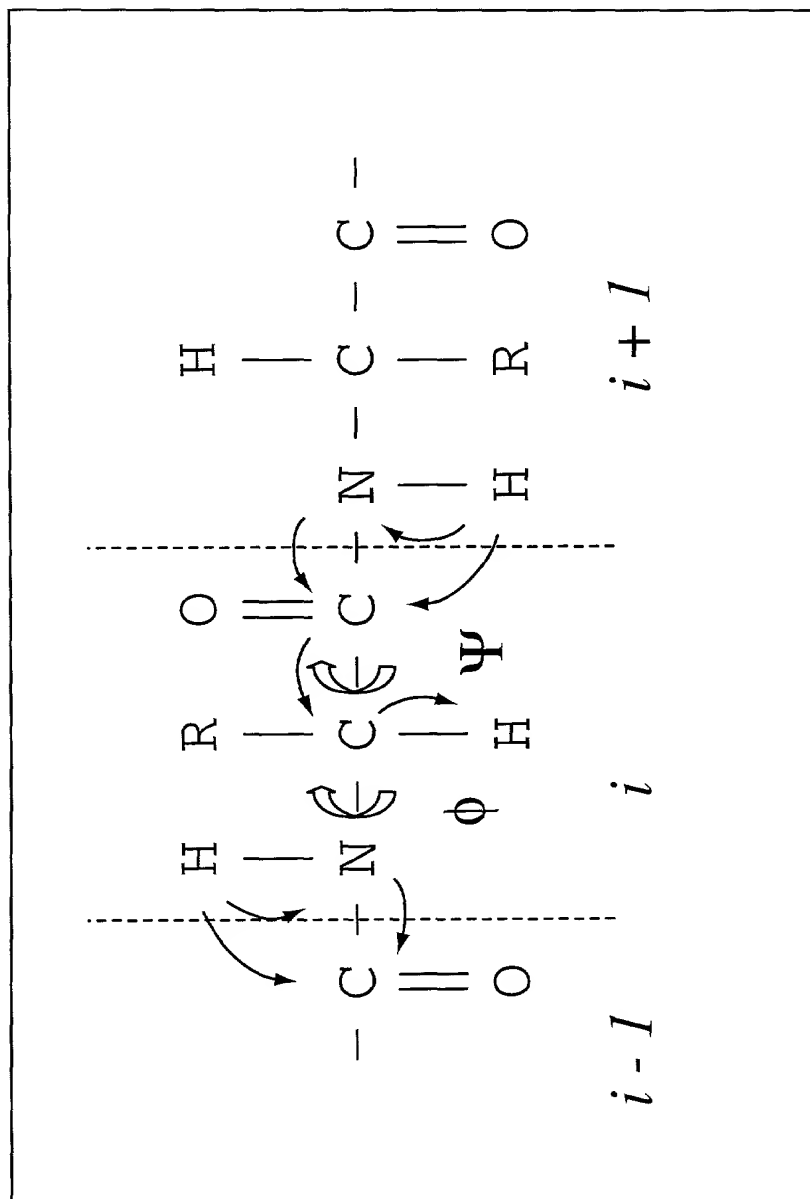


FIG. 2

205120 00000000

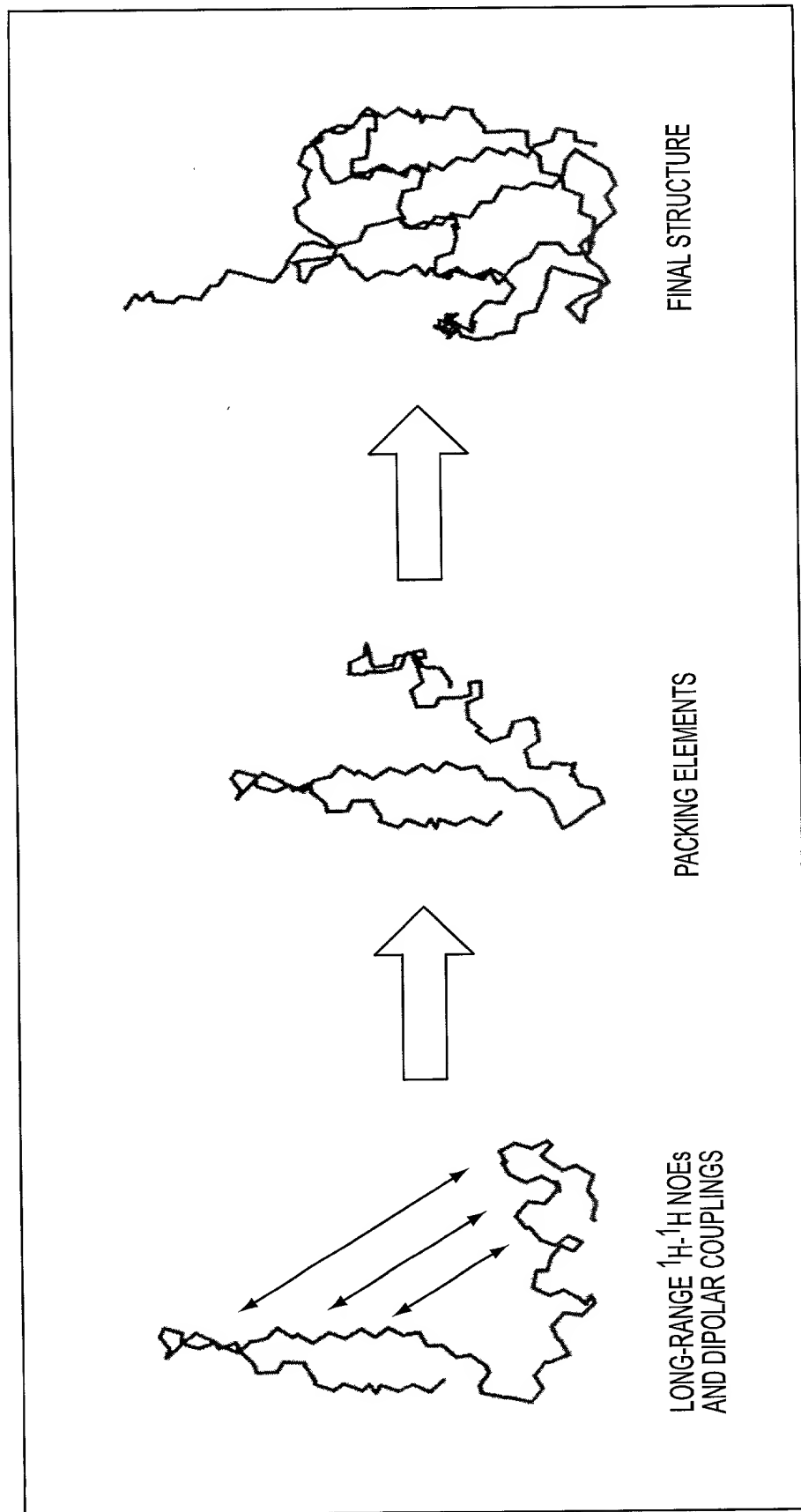
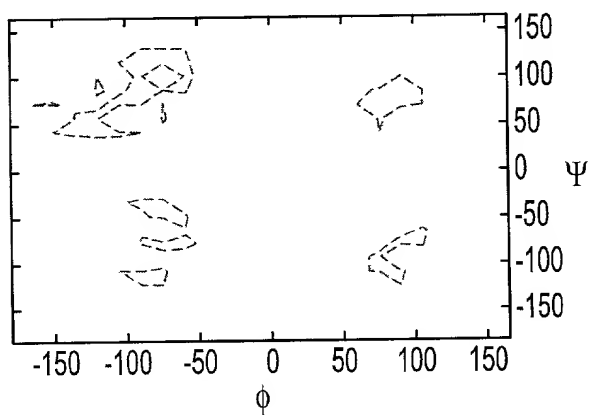
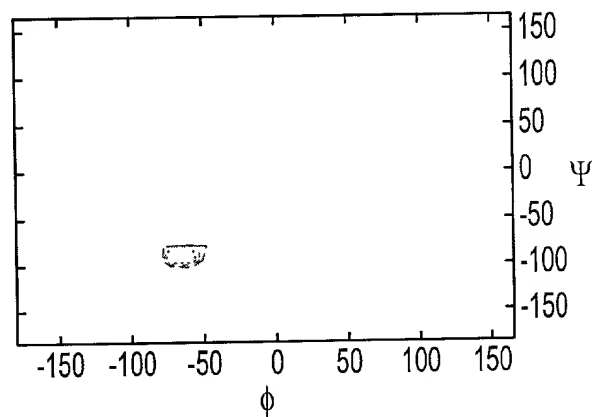
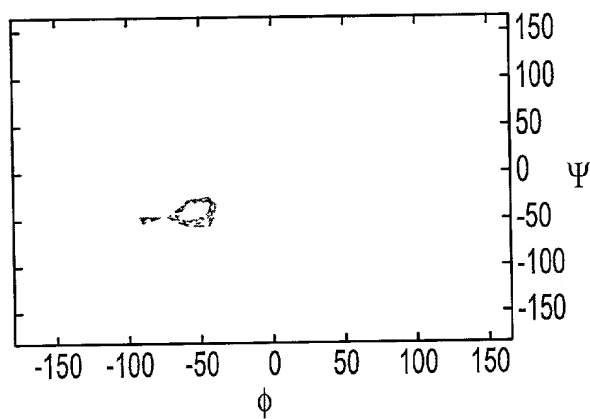
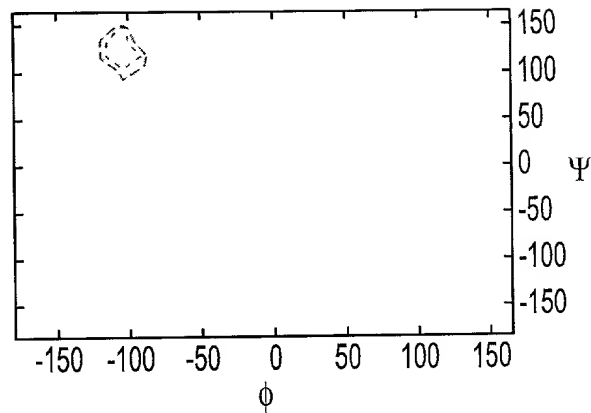
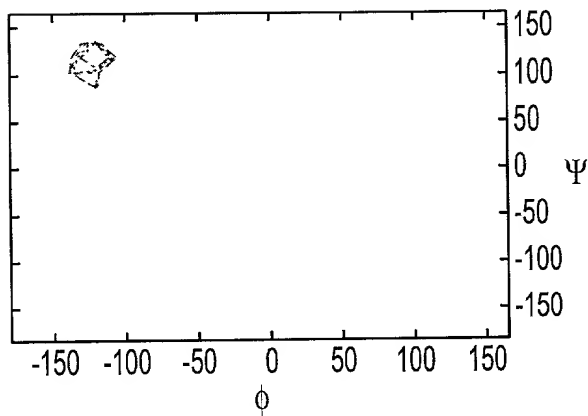


FIG. 3

205120" 020E3660



205120 02063650

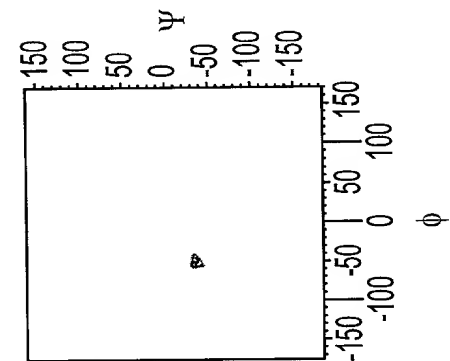


FIG. 5A

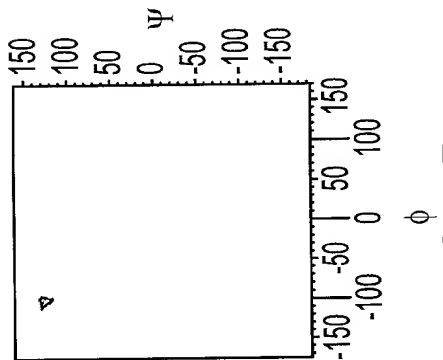


FIG. 5B

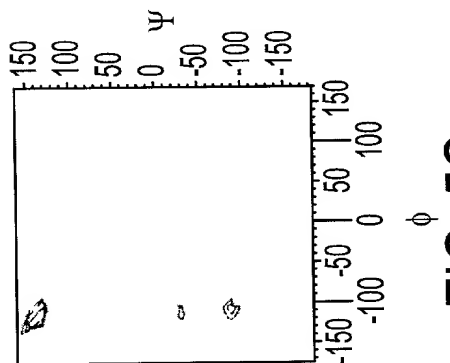


FIG. 5C

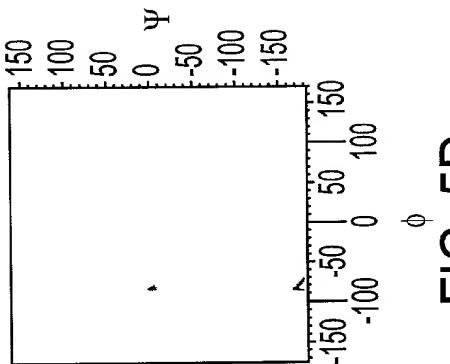


FIG. 5D

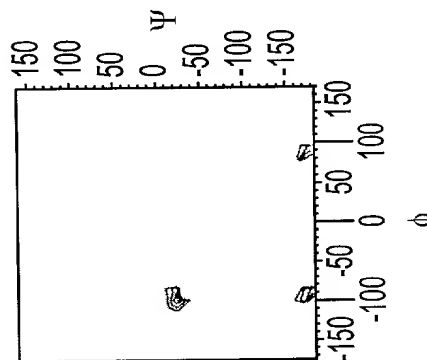


FIG. 5E

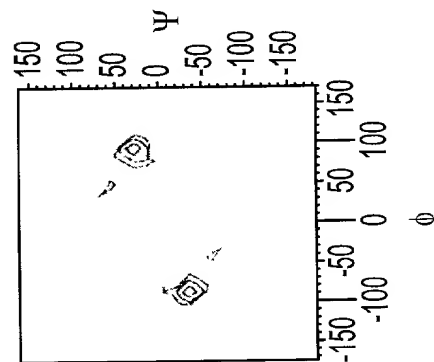


FIG. 5F

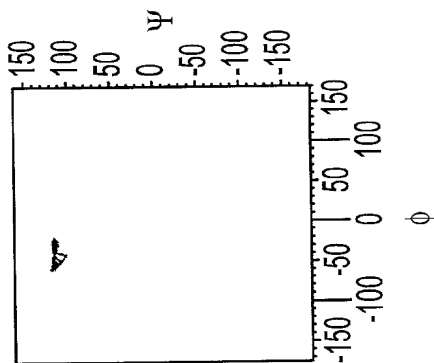


FIG. 5G

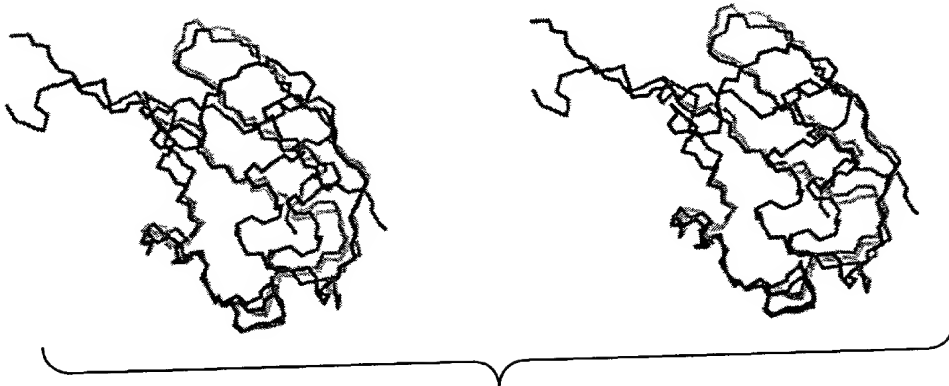


FIG. 6A

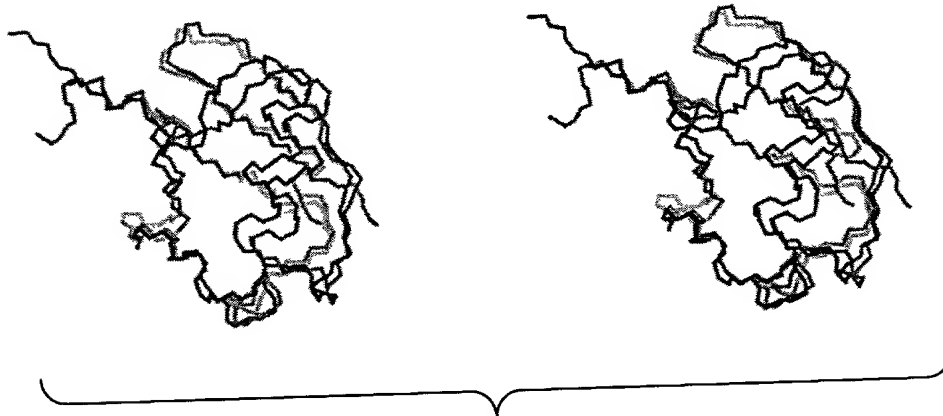


FIG. 6B

09983020-01507

GENERATE LINEAR  
AMINO-ACID CHAIN

CALCULATE  $\phi$ ,  $\psi$  ANGLES FOR  
EACH PEPTIDE PAIR USING  
EXPERIMENTAL RESIDUAL  
DIPOLAR COUPLINGS

FOLD LINEAR SEQUENCE WITH  
DIHEDRAL ANGLE AND  
BACKBONE NOE RESTRAINTS

REFINE STRUCTURE USING  
NOE AND DIPOLAR COUPLING  
RESTRAINTS

FIG. 7



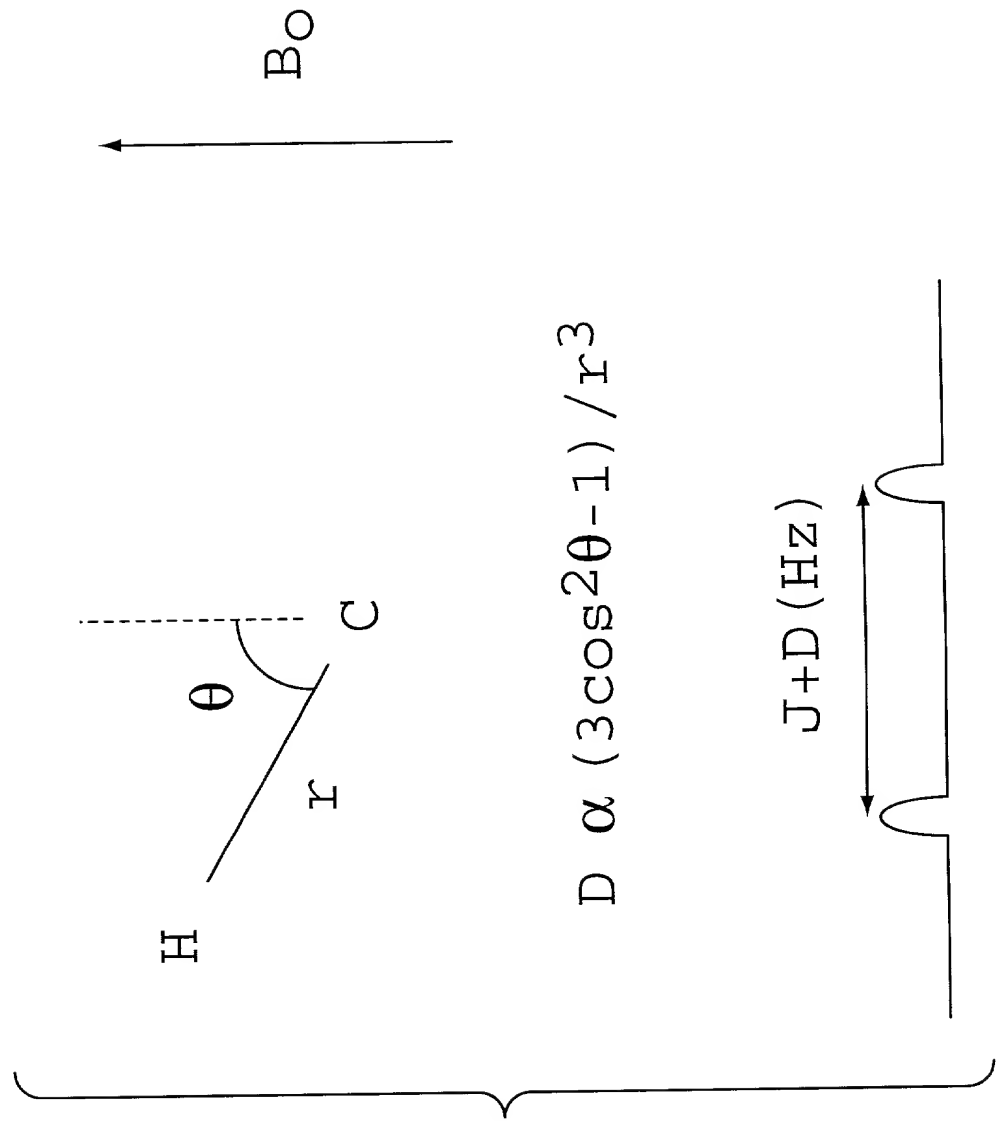


FIG. 8

205720" 020E8660

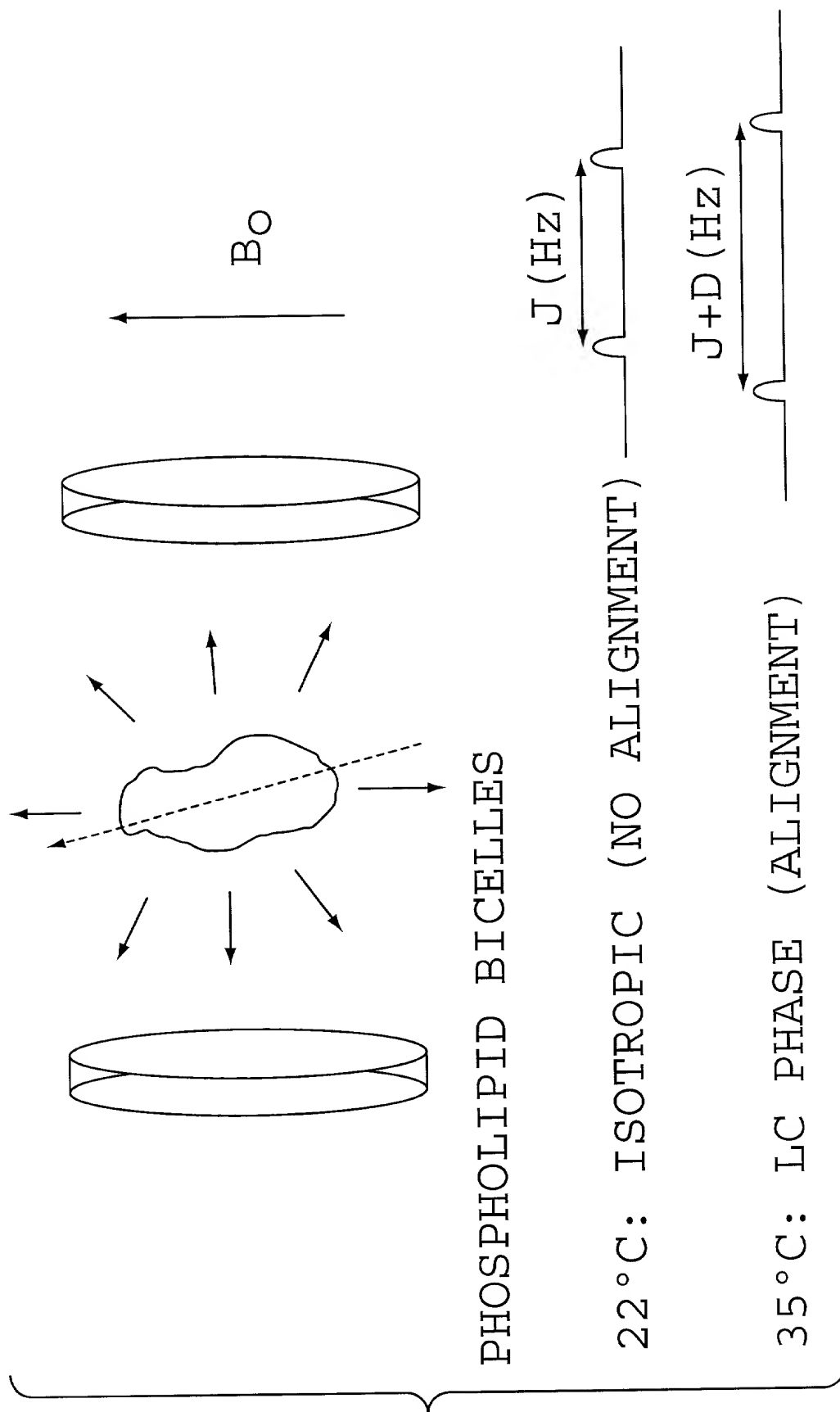
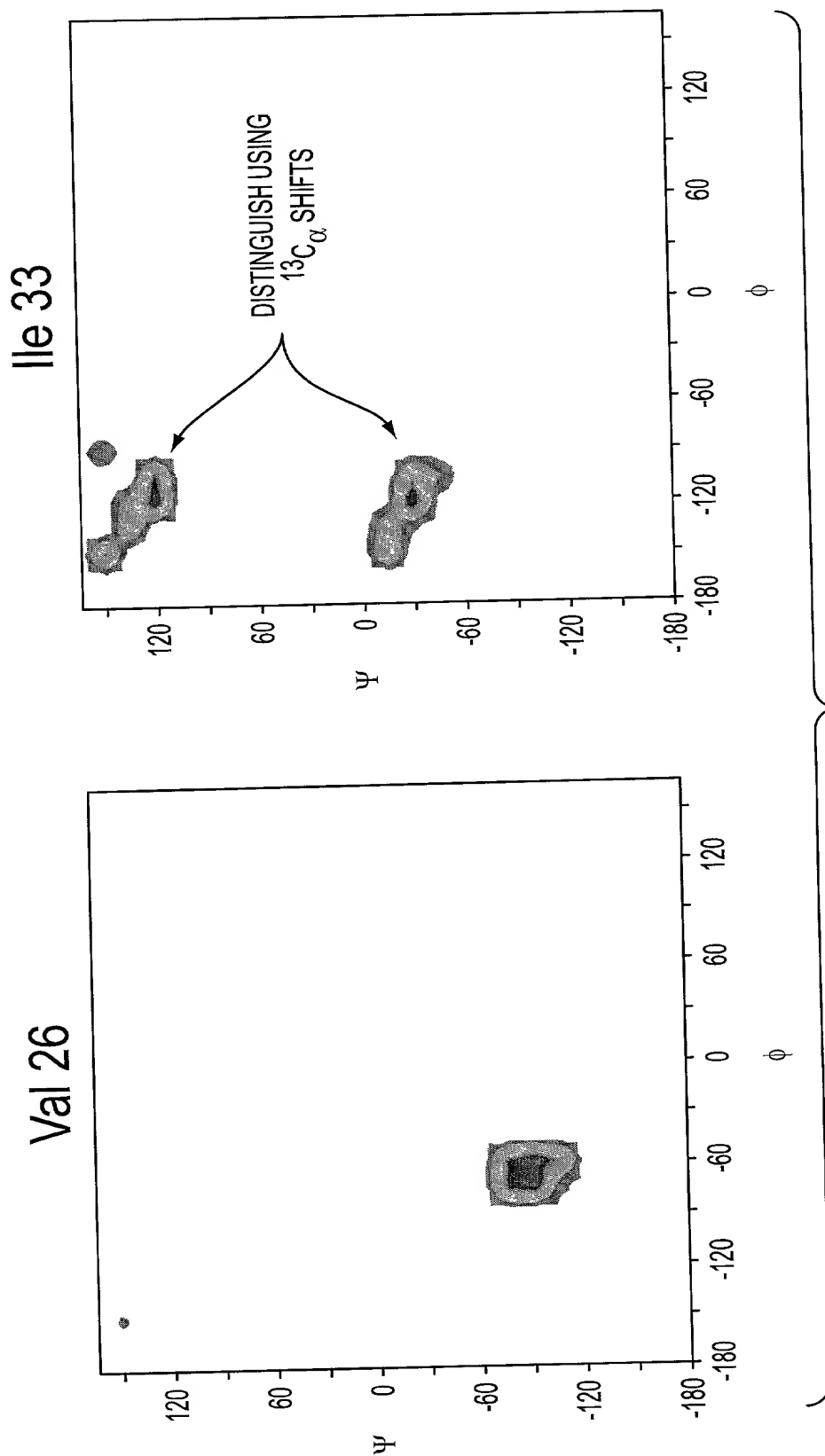


FIG. 9



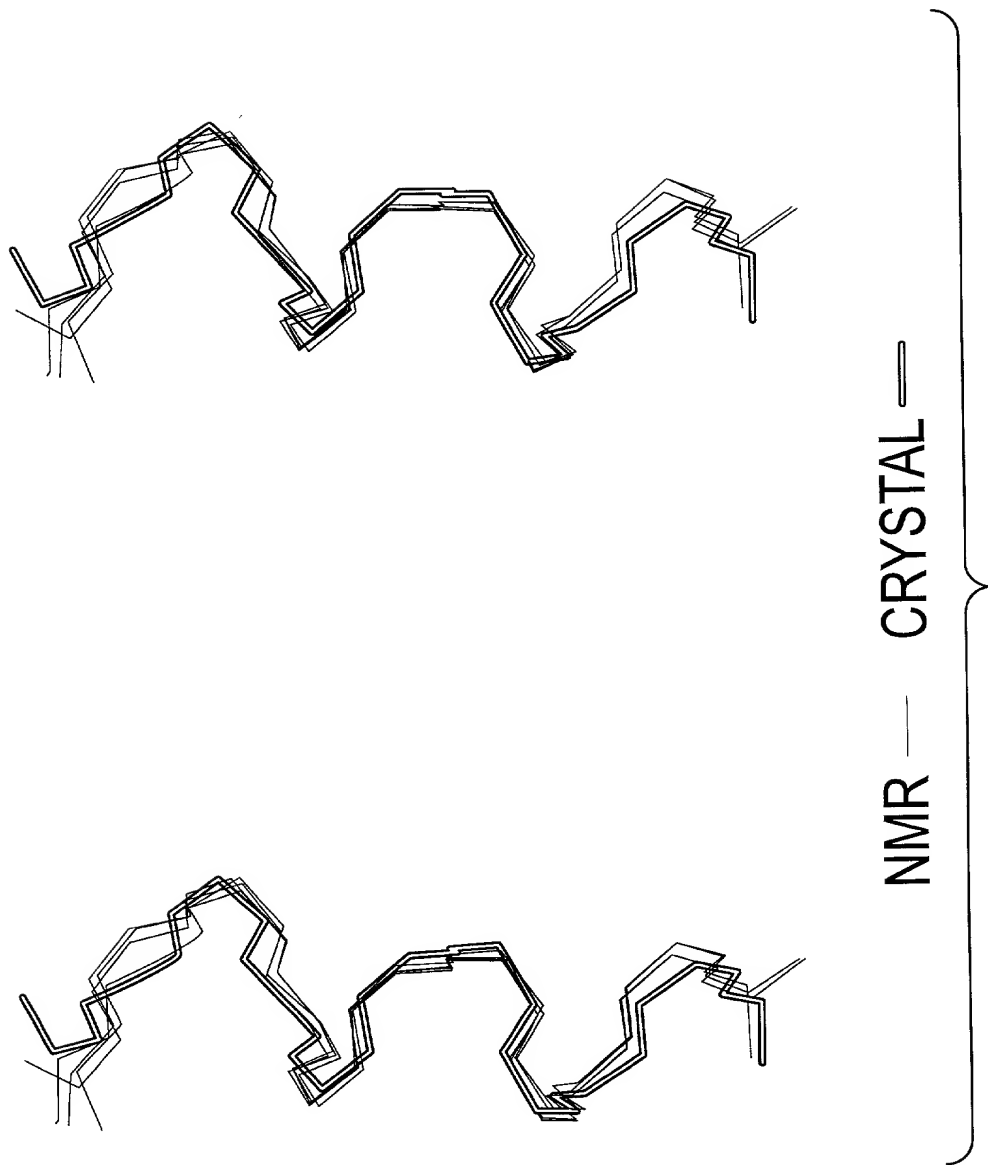


FIG. 11

205T20" 020E8660

0205120" 020513660

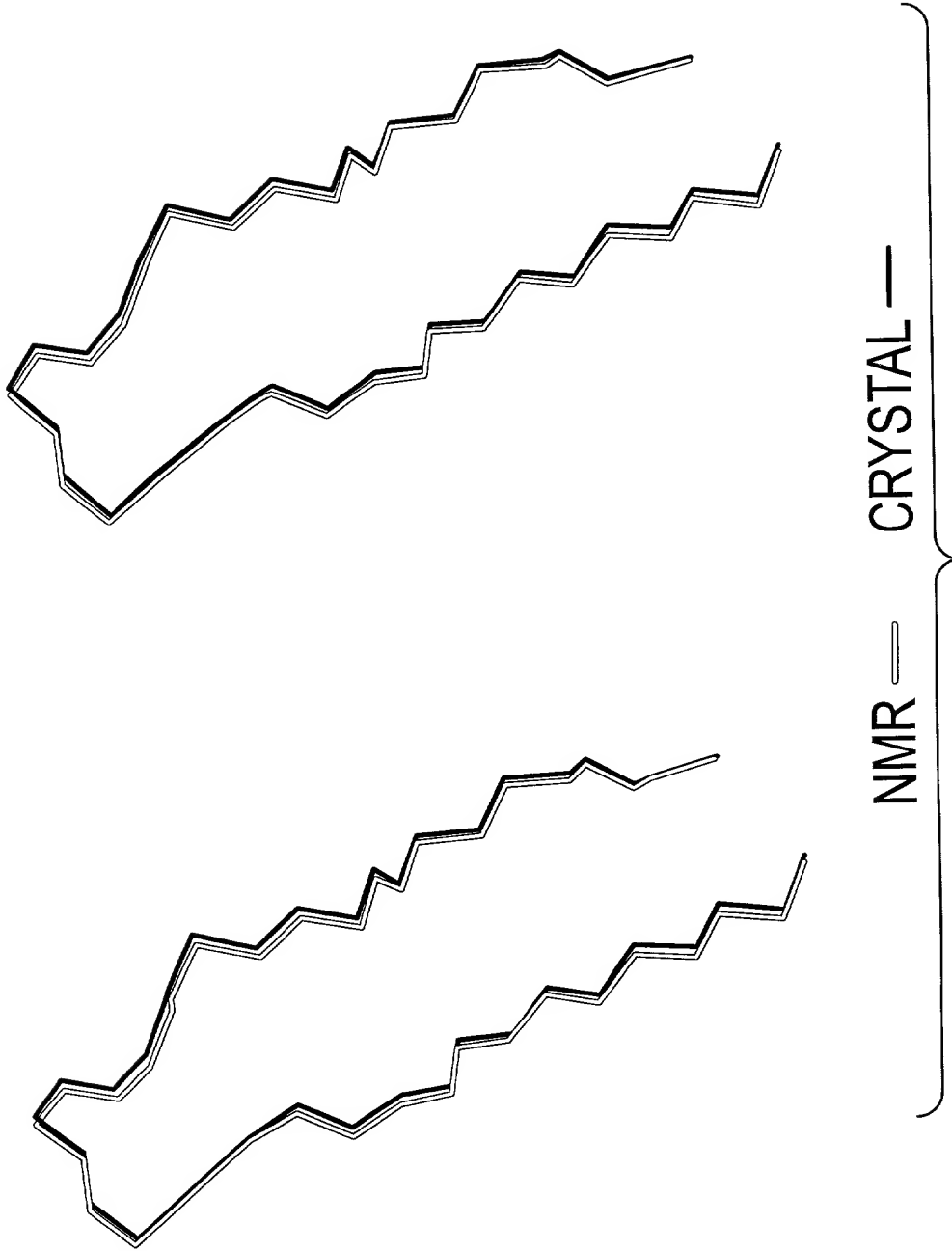


FIG. 12

205120" 02033660

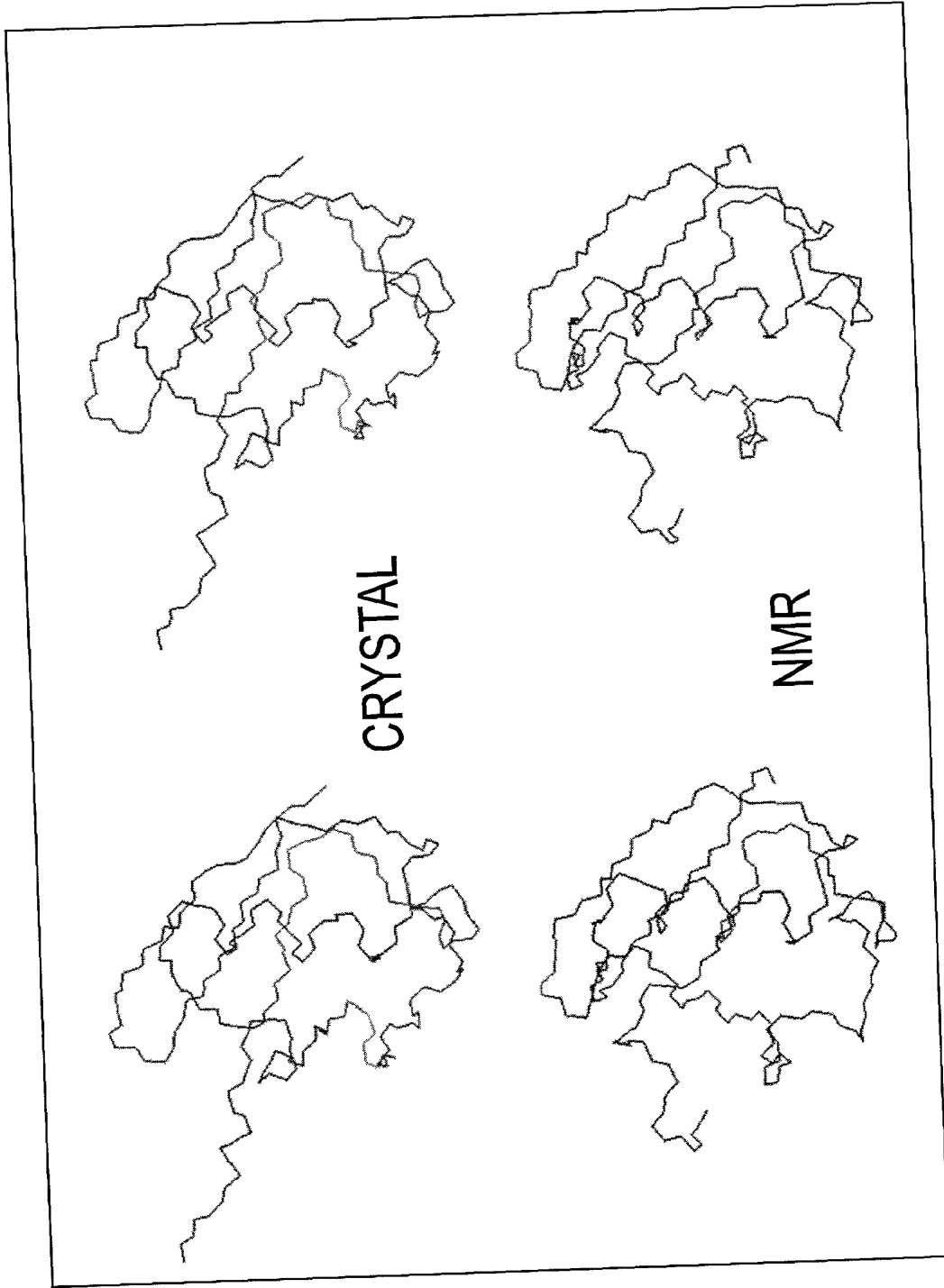


FIG. 13